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Sequence Listing was accepted.

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Reviewer: markspencer

Timestamp: [year=2008; month=10; day=24; hr=13; min=30; sec=35; ms=59; ]

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Application No: 10567091

Version No: 2.0

Input Set:

Output Set:

Started: 2008-09-25 12:59:17.733

Finished: 2008-09-25 12:59:22.458

Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 725 ms

Total Warnings: 42

Total Errors: 0

No. of SeqIDs Defined: 54

Actual SeqID Count: 54

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)

**Input Set:**

**Output Set:**

**Started:** 2008-09-25 12:59:17.733  
**Finished:** 2008-09-25 12:59:22.458  
**Elapsed:** 0 hr(s) 0 min(s) 4 sec(s) 725 ms  
**Total Warnings:** 42  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 54  
**Actual SeqID Count:** 54

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (35)
W 402	Undefined organism found in <213> in SEQ ID (36)
W 402	Undefined organism found in <213> in SEQ ID (37)
W 402	Undefined organism found in <213> in SEQ ID (38)
W 402	Undefined organism found in <213> in SEQ ID (39)
W 402	Undefined organism found in <213> in SEQ ID (40)

# SEQUENCE LISTING

<110> GRIESBECK, OLIVER  
HEIM, NICOLA

<120> NOVEL GENETICALLY ENCODED BIOINDICATORS OF CALCIUM-IONS

<130> 085449-0185

<140> 10567091

<141> 2008-09-25

<150> PCT/EP2004/008739

<151> 2004-08-04

<150> EP 03016691.2

<151> 2003-08-04

<160> 54

<170> PatentIn version 3.3

<210> 1

<211> 1863

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polynucleotide

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gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac	600
tacctgagca ccagtcgcg cctgagcaaa gaccccaacg agaagcgcg tcacatggtc	660
ctgctggagt tcgtgaccgc cgcccgcatg ctccgcgagg agatgattgc tgagttcaaa	720

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aacggcatca aggccaactt caagatccgc cacaacatcg aggacggcag cgtgcagctc	1680
gccgaccact accagcagaa ccccccatc ggcgacggcc ccgtgctgct gcccgacaac	1740
cactacctga gctaccagtc cgccctgagc aaagacccca acgagaagcg cgatcacatg	1800
gtcctgctgg agttcgtgac cgccgcggg atcactctcg gcatggacga gctgtacaag	1860
taa	1863

<210> 2

<211> 620

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polypeptide

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Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
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Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Arg	Phe	Ser	Val	Ser	Gly
			20					25						30	

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn  
145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
210 215 220

Val Thr Ala Ala Arg Met Leu Ser Glu Glu Met Ile Ala Glu Phe Lys  
225 230 235 240

Ala Ala Phe Asp Met Phe Asp Ala Asp Gly Gly Gly Asp Ile Ser Thr  
245 250 255

Lys Glu Leu Gly Thr Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys  
 260 265 270

Glu Glu Leu Asp Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly  
 275 280 285

Thr Ile Asp Phe Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys  
 290 295 300

Glu Asp Ala Lys Gly Lys Ser Glu Glu Glu Leu Ala Asn Cys Phe Arg  
 305 310 315 320

Ile Phe Asp Lys Asn Ala Asp Gly Phe Ile Asp Ile Glu Glu Leu Gly  
 325 330 335

Glu Ile Leu Arg Ala Thr Gly Glu His Val Ile Glu Glu Asp Ile Glu  
 340 345 350

Asp Leu Met Lys Asp Ser Asp Lys Asn Asn Asp Gly Arg Ile Asp Phe  
 355 360 365

Asp Glu Phe Leu Lys Met Met Glu Gly Val Gln Glu Leu Met Val Ser  
 370 375 380

Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu  
 385 390 395 400

Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu  
 405 410 415

Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr  
 420 425 430

Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr  
 435 440 445

Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln His Asp  
 450 455 460

Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile  
 465 470 475 480

Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe  
485 490 495

Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe  
500 505 510

Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn  
515 520 525

Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys  
530 535 540

Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu  
545 550 555 560

Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu  
565 570 575

Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp  
580 585 590

Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala  
595 600 605

Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
610 615 620

<210> 3

<211> 1902

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polynucleotide

<400> 3

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ggcaagctga ccttgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc	180
ctcgtgacca cctgacctg gggcgtgcag tgcttcagcc gctaccccga ccacatgaag	240
cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg taccatcttc	300
ttcaaggacg acggcaacta caagaccgc gccgaggtga agttcgaggg cgacaccctg	360



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aagctggagt	acaactacat	cagccacaac	gtctatatca	ccgccgacaa	gcagaagaac	480
ggcatcaagg	cccacttcaa	gatccgccac	aacatcgagg	acggcagcgt	gcagctcgcc	540
gaccactacc	agcagaacac	ccccatcggc	gacggccccg	tgctgctgcc	cgacaaccac	600
tacctgagca	cccagtcgcg	cctgagcaaa	gaccccaacg	agaagcgcg	tcacatggtc	660
ctgctggagt	togtgaccgc	cgcccgcatg	ctaattggatg	acatctacaa	ggctgcggta	720
gagcagctga	cagaagagca	gaaaaatgag	ttcaaggcag	ccttcgacat	cttcgtgctg	780
ggcgctgagg	atggctgcat	cagcaccaag	gagctgggca	aggtgatgag	gatgctgggc	840
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ggctacatcg	acctggatga	gctgaagata	atgctgcagg	ctacaggcga	gaccatcacg	1080
gaggacgaca	tcgaggaact	catgaaggac	ggagacaaga	acaacgacgg	ccgcatcgac	1140
tatgatgagt	tccctggagtt	catgaagggt	gtggaggagc	tcattggtgag	caagggcgag	1200
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aagggcatcg	acttcaagga	ggacggcaac	atcctggggc	acaagctgga	gtacaactac	1620
aacagccaca	acgtctatat	catggccgac	aagcagaaga	acggcatcaa	ggccaacttc	1680
aagatccgcc	acaacatcga	ggacggcagc	gtgcagctcg	ccgaccacta	ccagcagaac	1740
accccatcg	gcgacggccc	cgtgctgctg	cccgacaacc	actacctgag	ctaccagtcc	1800
gcctgagca	aagaccccaa	cgagaagcgc	gatcacatgg	tctgctgga	gttcgtgacc	1860
gccgcgggga	tactctcgg	catggacgag	ctgtacaagt	aa		1902

<210> 4

<211> 633

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polypeptide

<400> 4

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
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Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Arg	Phe	Ser	Val	Ser	Gly
	20						25					30			

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
	35						40					45			

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
	50					55					60				

Leu	Thr	Trp	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys
65					70					75				80	

Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
			85						90					95	

Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
			100					105						110	

Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
		115					120					125			

Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
	130					135					140				

Asn	Tyr	Ile	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn
145					150					155				160	

Gly	Ile	Lys	Ala	His	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser
			165						170					175	

Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly
		180						185					190		

Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu
		195					200						205		

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
210 215 220

Val Thr Ala Ala Arg Met Leu Met Asp Asp Ile Tyr Lys Ala Ala Val  
225 230 235 240

Glu Gln Leu Thr Glu Glu Gln Lys Asn Glu Phe Lys Ala Ala Phe Asp  
245 250 255

Ile Phe Val Leu Gly Ala Glu Asp Gly Cys Ile Ser Thr Lys Glu Leu  
260 265 270

Gly Lys Val Met Arg Met Leu Gly Gln Asn Pro Thr Pro Glu Glu Leu  
275 280 285

Gln Glu Met Ile Asp Glu Val Asp Glu Asp Gly Ser Gly Thr Val Asp  
290 295 300

Phe Asp Glu Phe Leu Val Met Met Val Arg Cys Met Lys Asp Asp Ser  
305 310 315 320

Lys Gly Lys Ser Glu Glu Glu Leu Ser Asp Leu Phe Arg Met Phe Asp  
325 330 335

Lys Asn Ala Asp Gly Tyr Ile Asp Leu Asp Glu Leu Lys Ile Met Leu  
340 345 350

Gln Ala Thr Gly Glu Thr Ile Thr Glu Asp Asp Ile Glu Glu Leu Met  
355 360 365

Lys Asp Gly Asp Lys Asn Asn Asp Gly Arg Ile Asp Tyr Asp Glu Phe  
370 375 380

Leu Glu Phe Met Lys Gly Val Glu Glu Leu Met Val Ser Lys Gly Glu  
385 390 395 400

Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp  
405 410 415

Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala  
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Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu  
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Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met  
450 455 460

Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln His Asp Phe Phe Lys  
465 470 475 480

Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys  
485 490 495

Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp  
500 505 510

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp  
515 520 525

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn  
530 535 540

Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe  
545 550 555 560

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His  
565 570 575

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp  
580 585 590

Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu  
595 600 605

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile  
610 615 620

Thr Leu Gly Met Asp Glu Leu Tyr Lys  
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<210> 5

<211> 1863

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polynucleotide

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ggcaagctga cctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc	180
ctcgtgacca cctgacctg gggcgtgcag tgcttcagcc gctaccccgga ccacatgaag	240
cagcacgact ttttcaagtc cgccatgccc gaaggetacg tccaggagcg taccatcttc	300
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gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac	600
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